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SEQUENCE LISTING

<110> Aventis Pasteur Limited
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 Raudonikiene, Ausra
 Gallichan, Scott
 Murdin, Andrew

<120> Immunization Against Chlamydia Infectio with 60K CRMP

<130> RY185

<150> US 60/481,676
 <151> 2003-11-20

<160> 14

<170> PatentIn version 3.3

<210> 1
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 <212> DNA
 <213> Chlamydia muridium

<220>
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 <222> (1)..(1662)

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atc ttc gcg gtg act agt gtg gcg agt tta ttt gct agc ggg gtg tta	96
Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu	
20 25 30	
gag acc tct atg gca gag tct ctc tct acc aac gtt att agc tta gct	144
Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala	
35 40 45	
gac acc aaa gcg aaa gag acc act tct cat caa aaa gac aga aaa gca	192
Asp Thr Lys Ala Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala	
50 55 60	
aga aaa aat cat caa aat agg act tcc gta gtc cgt aaa gag gtt act	240
Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr	
65 70 75 80	
gca gtt cgt gat act aaa gct gta gag cct aga cag gat tct tgc ttt	288
Ala Val Arg Asp Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe	
85 90 95	
ggc aaa atg tat aca gtc aaa gtt aat gat gat cgt aat gta gaa atc	336
Gly Lys Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile	

100	105	110	
gtg cag tcc gtt cct gaa tat gct acg gta gga tct cca tat cct att Val Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile 115 120 125			384
gag att act gct ata ggg aaa aga gac tgt gtt gat gta atc att aca Glu Ile Thr Ala Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr 130 135 140			432
cag caa tta cca tgc gaa gca gag ttt gtt agc agt gat cca gct act Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr 145 150 155 160			480
act cct act gct gat ggt aag cta gtt tgg aaa att gat cgg tta gga Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly 165 170 175			528
cag ggc gaa aag agt aaa att act gta tgg gta aaa cct ctt aaa gaa Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu 180 185 190			576
ggt tgc tgc ttt aca gct gca acg gtt tgt gct tgt cca gag atc cgt Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg 195 200 205			624
tcg gtt acg aaa tgt ggc cag cct gct atc tgt gtt aaa cag gaa ggt Ser Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly 210 215 220			672
cca gaa agc gca tgt ttg cgt tgc cca gta act tat aga att aat gta Pro Glu Ser Ala Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val 225 230 235 240			720
gtc aac caa gga aca gca aca gca cgt aat gtt gtt gtg gaa aat cct Val Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro 245 250 255			768
gtt cca gat ggc tat gct cat gca tcc gga cag cgt gta ttg aca tat Val Pro Asp Gly Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr 260 265 270			816
act ctt ggg gat atg caa cct gga gaa cag aga aca atc acc gtg gag Thr Leu Gly Asp Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu 275 280 285			864
ttt tgt ccg ctt aaa cgt ggt cga gtc aca aat att gct aca gtt tct Phe Cys Pro Leu Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser 290 295 300			912
tac tgt ggt gga cac aaa aat act gct agc gta aca aca gtg atc aat Tyr Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn 305 310 315 320			960
gag cct tgc gtg caa gtt aac atc gag gga gca gat tgg tct tat gtt Glu Pro Cys Val Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val 325 330 335			1008

tgt aag cct gta gaa tat gtt atc tct gtt tct aac cct ggt gac tta Cys Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu 340 345 350	1056
gtt tta cga gac gtt gta att gaa gat acg ctt tct cct gga ata act Val Leu Arg Asp Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr 355 360 365	1104
gtt gtt gaa gca gct gga gct cag att tct tgt aat aaa ttg gtt tgg Val Val Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp 370 375 380	1152
act ttg aag gaa ctc aat cct gga gag tct tta caa tat aag gtt cta Thr Leu Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu 385 390 395 400	1200
gta aga gct caa act cca ggg caa ttc aca aac aac gtt gtt gtg aaa Val Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys 405 410 415	1248
agt tgc tct gat tgc ggt att tgt act tct tgc gca gaa gca aca act Ser Cys Ser Asp Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr 420 425 430	1296
tac tgg aaa gga gtt gct gct act cat atg tgc gta gta gat act tgt Tyr Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys 435 440 445	1344
gat cct att tgc gta gga gag aac act gtt tat cgt atc tgt gtg aca Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr 450 455 460	1392
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aaa gaa act gta gag ttt tct gta acg ttg aaa gca gta tcc gct gga Lys Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly 515 520 525	1584
gat gct cgt ggg gaa gct att ctt tct tcc gat aca ttg aca gtt cct Asp Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro 530 535 540	1632
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 <213> Chlamydia muridium

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Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
 35 40 45

Asp Thr Lys Ala Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala
 50 55 60

Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr
 65 70 75 80

Ala Val Arg Asp Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe
 85 90 95

Gly Lys Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile
 100 105 110

Val Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile
 115 120 125

Glu Ile Thr Ala Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr
 130 135 140

Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr
 145 150 155 160

Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly
 165 170 175

Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu
 180 185 190

Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg

195 200 205
 Ser Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly
 210 215 220
 Pro Glu Ser Ala Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val
 225 230 235 240
 Val Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro
 245 250 255
 Val Pro Asp Gly Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr
 260 265 270
 Thr Leu Gly Asp Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu
 275 280 285
 Phe Cys Pro Leu Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser
 290 295 300
 Tyr Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn
 305 310 315 320
 Glu Pro Cys Val Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val
 325 330 335
 Cys Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu
 340 345 350
 Val Leu Arg Asp Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr
 355 360 365
 Val Val Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp
 370 375 380
 Thr Leu Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu
 385 390 395 400
 Val Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys
 405 410 415
 Ser Cys Ser Asp Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr
 420 425 430

Tyr Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys
435 440 445

Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr
450 455 460

Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe
465 470 475 480

Ser Lys Glu Leu Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr
485 490 495

Ile Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser
500 505 510

Lys Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly
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Val Ser Asp Thr Glu Asn Thr His Ile Tyr
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atc ttc gcg gtg act agt gtg gcg agt tta ttt gct agc ggg gtg tta 96
Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu
20 25 30

gag acc tct atg gca gag tct ctc tct aca aac gtt att agc tta gct 144
Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
35 40 45

gac acc aaa gcg aaa gac aac act tct cat aaa agc aaa aaa gca aga Asp Thr Lys Ala Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg 50 55 60	192
aaa aac cac agc aaa gag act ccc gta gac cgt aaa gag gtt gct ccg Lys Asn His Ser Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro 65 70 75 80	240
gtt cat gag tct aaa gct aca gga cct aaa cag gat tct tgc ttt ggc Val His Glu Ser Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly 85 90 95	288
aga atg tat aca gtc aaa gtt aat gat gat cgc aat gtt gaa atc aca Arg Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr 100 105 110	336
caa gct gtt cct gaa tat gct acg gta gga tct ccc tat cct att gaa Gln Ala Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu 115 120 125	384
att act gct aca ggt aaa agg gat tgt gtt gat gtt atc att act cag Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln 130 135 140	432
caa tta cca tgt gaa gca gag ttc gta cgc agt gat cca gcg aca act Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr 145 150 155 160	480
cct act gct gat ggt aag cta gtt tgg aaa att gac cgc tta gga caa Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln 165 170 175	528
ggc gaa aag agt aaa att act gta tgg gta aaa cct ctt aaa gaa ggt Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly 180 185 190	576
tgc tgc ttt aca gct gca aca gta tgc gct tgt cca gag atc cgt tcg Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser 195 200 205	624
gtt aca aaa tgt gga caa cct gct atc tgt gtt aaa caa gaa ggc cca Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro 210 215 220	672
gag aat gct tgt ttg cgt tgc cca gta gtt tac aaa att aat ata gtg Glu Asn Ala Cys Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val 225 230 235 240	720
aac caa gga aca gca aca gct cgt aac gtt gtt gtt gaa aat cct gtt Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val 245 250 255	768
cca gat ggt tac gct cat tct tct gga cag cgt gta ctg acg ttt act Pro Asp Gly Tyr Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr 260 265 270	816
ctt gga gat atg caa cct gga gag cac aga aca att act gta gag ttt	864

Leu Gly Asp Met Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe	
275 280 285	
tgt ccg ctt aaa cgt ggt cgt gct acc aat ata gca acg gtt tct tac	912
Cys Pro Leu Lys Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr	
290 295 300	
tgt gga gga cat aaa aat aca gca agc gta aca act gtg atc aac gag	960
Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu	
305 310 315 320	
cct tgc gta caa gta agt att gca gga gca gat tgg tct tat gtt tgt	1008
Pro Cys Val Gln Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys	
325 330 335	
aag cct gta gaa tat gtg atc tcc gtt tcc aat cct gga gat ctt gtg	1056
Lys Pro Val Gly Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val	
340 345 350	
ttg cga gat gtc gtc gtt gaa gac act ctt tct ccc gga gtc aca gtt	1104
Leu Arg Asp Val Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val	
355 360 365	
ctt gaa gct gca gga gct caa att tct tgt aat aaa gta gtt tgg act	1152
Leu Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr	
370 375 380	
gtg aaa gaa ctg aat cct gga gag tct cta cag tat aaa gtt cta gta	1200
Val Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val	
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aga gca caa act cct gga caa ttc aca aat aat gtt gtt gtg aag agc	1248
Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser	
405 410 415	
tgc tct gac tgt ggt act tgt act tct tgc gca gaa gcg aca act tac	1296
Cys Ser Asp Cys Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr	
420 425 430	
tgg aaa gga gtt gct gct act cat atg tgc gta gta gat act tgt gac	1344
Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp	
435 440 445	
cct gtt tgt gta gga gaa aat act gtt tac cgt att tgt gtc acc aac	1392
Pro Val Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn	
450 455 460	
aga ggt tct gca gaa gat aca aat gtt tct tta atg ctt aaa ttc tct	1440
Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser	
465 470 475 480	
aaa gaa ctg caa cct gta tcc ttc tct gga cca act aaa gga acg att	1488
Lys Glu Leu Gln Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile	
485 490 495	
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515	520	525	
gct cgt ggg gaa gcg att ctt tct tcc gat aca ttg act gtt cca gtt			1632
Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val			
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35 40 45

Asp Thr Lys Ala Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg
50 55 60

Lys Asn His Ser Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro
65 70 75 80

Val His Glu Ser Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly
85 90 95

Arg Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr
100 105 110

Gln Ala Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu
115 120 125

Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln
130 135 140

Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr
 145 150 155 160
 Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln
 165 170 175
 Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly
 180 185 190
 Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser
 195 200 205
 Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro
 210 215 220
 Glu Asn Ala Cys Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val
 225 230 235 240
 Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val
 245 250 255
 Pro Asp Gly Tyr Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr
 260 265 270
 Leu Gly Asp Met Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe
 275 280 285
 Cys Pro Leu Lys Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr
 290 295 300
 Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu
 305 310 315 320
 Pro Cys Val Gln Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys
 325 330 335
 Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val
 340 345 350
 Leu Arg Asp Val Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val
 355 360 365

Leu Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr
 370 375 380

Val Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val
 385 390 395 400

Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser
 405 410 415

Cys Ser Asp Cys Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr
 420 425 430

Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp
 435 440 445

Pro Val Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn
 450 455 460

Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser
 465 470 475 480

Lys Glu Leu Gln Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile
 485 490 495

Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys
 500 505 510

Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp
 515 520 525

Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val
 530 535 540

Ser Asp Thr Glu Asn Thr His Ile Tyr
 545 550

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 Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala Arg Lys Asn His
 20 25 30

caa aat agg act tcc gta gtc cgt aaa gag gtt act gca gtt cgt gat 144
 Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr Ala Val Arg Asp
 35 40 45

act aaa gct gta gag cct aga cag gat tct tgc ttt ggc aaa atg tat 192
 Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe Gly Lys Met Tyr
 50 55 60

aca gtc aaa gtt aat gat gat cgt aat gta gaa atc gtg cag tcc gtt 240
 Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Val Gln Ser Val
 65 70 75 80

cct gaa tat gct acg gta gga tct cca tat cct att gag att act gct 288
 Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala
 85 90 95

ata ggg aaa aga gac tgt gtt gat gta atc att aca cag caa tta cca 336
 Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro
 100 105 110

tgc gaa gca gag ttt gtt agc agt gat cca gct act act cct act gct 384
 Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr Thr Pro Thr Ala
 115 120 125

gat ggt aag cta gtt tgg aaa att gat cgg tta gga cag ggc gaa aag 432
 Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys
 130 135 140

agt aaa att act gta tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttt 480
 Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe
 145 150 155 160

aca gct gca acg gtt tgt gct tgt cca gag atc cgt tgc gtt acg aaa 528
 Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys
 165 170 175

tgt ggc cag cct gct atc tgt gtt aaa cag gaa ggt cca gaa agc gca 576
 Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Ser Ala
 180 185 190

tgt ttg cgt tgc cca gta act tat aga att aat gta gtc aac caa gga 624
 Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val Val Asn Gln Gly
 195 200 205

aca gca aca gca cgt aat gtt gtt gtg gaa aat cct gtt cca gat ggc 672
 Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly
 210 215 220

tat gct cat gca tcc gga cag cgt gta ttg aca tat act ctt ggg gat	720
Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr Thr Leu Gly Asp	
225 230 235 240	
atg caa cct gga gaa cag aga aca atc acc gtg gag ttt tgt ccg ctt	768
Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu Phe Cys Pro Leu	
245 250 255	
aaa cgt ggt cga gtc aca aat att gct aca gtt tct tac tgt ggt gga	816
Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly	
260 265 270	
cac aaa aat act gct agc gta aca aca gtg atc aat gag cct tgc gtg	864
His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val	
275 280 285	
caa gtt aac atc gag gga gca gat tgg tct tat gtt tgt aag cct gta	912
Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val	
290 295 300	
gaa tat gtt atc tct gtt tct aac cct ggt gac tta gtt tta cga gac	960
Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp	
305 310 315 320	
gtt gta att gaa gat acg ctt tct cct gga ata act gtt gtt gaa gca	1008
Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr Val Val Glu Ala	
325 330 335	
gct gga gct cag att tct tgt aat aaa ttg gtt tgg act ttg aag gaa	1056
Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp Thr Leu Lys Glu	
340 345 350	
ctc aat cct gga gag tct tta caa tat aag gtt cta gta aga gct caa	1104
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Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp	
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Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly	
385 390 395 400	
gtt gct gct act cat atg tgc gta gta gat act tgt gat cct att tgc	1248
Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Ile Cys	
405 410 415	
gta gga gag aac act gtt tat cgt atc tgt gtg aca aac aga ggt tct	1296
Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser	
420 425 430	
gct gaa gat aca aat gtg tcc tta att ttg aaa ttc tct aaa gaa tta	1344
Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu	
435 440 445	

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 Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn
 450 455 460

acg gta gtg ttt gat tct tta cct aga tta ggt tct aaa gaa act gta 1440
 Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val
 465 470 475 480

gag ttt tct gta acg ttg aaa gca gta tcc gct gga gat gct cgt ggg 1488
 Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly
 485 490 495

gaa gct att ctt tct tcc gat aca ttg aca gtt cct gta tct gat acg 1536
 Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr
 500 505 510

gag aat aca cat atc tat 1554
 Glu Asn Thr His Ile Tyr
 515

<210> 6

<211> 518

<212> PRT

<213> Chlamydia muridum

<400> 6

Met Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala Asp Thr Lys Ala
 1 5 10 15

Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala Arg Lys Asn His
 20 25 30

Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr Ala Val Arg Asp
 35 40 45

Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe Gly Lys Met Tyr
 50 55 60

Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Val Gln Ser Val
 65 70 75 80

Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala
 85 90 95

Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro
 100 105 110

Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr Thr Pro Thr Ala

115	120	125
Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys		
130	135	140
Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe		
145	150	155 160
Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys		
	165	170 175
Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Ser Ala		
	180	185 190
Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val Val Asn Gln Gly		
	195	200 205
Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly		
	210	215 220
Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr Thr Leu Gly Asp		
225	230	235 240
Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu Phe Cys Pro Leu		
	245	250 255
Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly		
	260	265 270
His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val		
	275	280 285
Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val		
	290	295 300
Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp		
305	310	315 320
Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr Val Val Glu Ala		
	325	330 335
Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp Thr Leu Lys Glu		
	340	345 350

Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln
 355 360 365

Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp
 370 375 380

Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly
 385 390 395 400

Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Ile Cys
 405 410 415

Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser
 420 425 430

Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu
 435 440 445

Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn
 450 455 460

Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val
 465 470 475 480

Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly
 485 490 495

Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr
 500 505 510

Glu Asn Thr His Ile Tyr
 515

<210> 7
 <211> 1551
 <212> DNA
 <213> Chlamydia trachomatis

<220>
 <221> CDS
 <222> (1)..(1551)

<400> 7

atg gag tct ctc tct aca aac gtt att agc tta gct gac acc aaa gcg Met Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala Asp Thr Lys Ala 1 5 10 15	48
aaa gac aac act tct cat aaa agc aaa aaa gca aga aaa aac cac agc Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg Lys Asn His Ser 20 25 30	96
aaa gag act ccc gta gac cgt aaa gag gtt gct ccg gtt cat gag tct Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro Val His Glu Ser 35 40 45	144
aaa gct aca gga cct aaa cag gat tct tgc ttt ggc aga atg tat aca Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly Arg Met Tyr Thr 50 55 60	192
gtc aaa gtt aat gat gat cgc aat gtt gaa atc aca caa gct gtt cct Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr Gln Ala Val Pro 65 70 75 80	240
gaa tat gct acg gta gga tct ccc tat cct att gaa att act gct aca Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala Thr 85 90 95	288
ggc aaa agg gat tgt gtt gat gtt atc att act cag caa tta cca tgt Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys 100 105 110	336
gaa gca gag ttc gta cgc agt gat cca gcg aca act cct act gct gat Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp 115 120 125	384
ggc aag cta gtt tgg aaa att gac cgc tta gga caa ggc gaa aag agt Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser 130 135 140	432
aaa att act gta tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttt aca Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr 145 150 155 160	480
gct gca aca gta tgc gct tgt cca gag atc cgt tcg gtt aca aaa tgt Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys Cys 165 170 175	528
gga caa cct gct atc tgt gtt aaa caa gaa ggc cca gag aat gct tgt Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Asn Ala Cys 180 185 190	576
ttg cgt tgc cca gta gtt tac aaa att aat ata gtg aac caa gga aca Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val Asn Gln Gly Thr 195 200 205	624
gca aca gct cgt aac gtt gtt gtt gaa aat cct gtt cca gat ggt tac Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly Tyr 210 215 220	672
gct cat tct tct gga cag cgt gta ctg acg ttt act ctt gga gat atg	720

SUBSTITUTE SHEET (RULE 26)

450 455 460

gta gta ttc gat tcg tta cct aga tta ggt tct aaa gaa act gta gag 1440
 Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val Glu
 465 470 475 480

ttt tct gta aca ttg aaa gca gta tca gct gga gat gct cgt ggg gaa 1488
 Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly Glu
 485 490 495

gcg att ctt tct tcc gat aca ttg act gtt cca gtt tct gat aca gag 1536
 Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr Glu
 500 505 510

aat aca cac atc tat 1551
 Asn Thr His Ile Tyr
 515

<210> 8
 <211> 517
 <212> PRT
 <213> Chlamydia trachomatis

<400> 8

Met Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala Asp Thr Lys Ala
 1 5 10 15

Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg Lys Asn His Ser
 20 25 30

Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro Val His Glu Ser
 35 40 45

Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly Arg Met Tyr Thr
 50 55 60

Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr Gln Ala Val Pro
 65 70 75 80

Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala Thr
 85 90 95

Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys
 100 105 110

Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp
 115 120 125

Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser
 130 135 140

Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr
 145 150 155 160

Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys Cys
 165 170 175

Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Asn Ala Cys
 180 185 190

Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val Asn Gln Gly Thr
 195 200 205

Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly Tyr
 210 215 220

Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr Leu Gly Asp Met
 225 230 235 240

Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe Cys Pro Leu Lys
 245 250 255

Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly His
 260 265 270

Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val Gln
 275 280 285

Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val Glu
 290 295 300

Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp Val
 305 310 315 320

Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val Leu Glu Ala Ala
 325 330 335

Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr Val Lys Glu Leu
 340 345 350

Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln Thr
 355 360 365

Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp Cys
 370 375 380

Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly Val
 385 390 395 400

Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Val Cys Val
 405 410 415

Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala
 420 425 430

Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser Lys Glu Leu Gln
 435 440 445

Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn Thr
 450 455 460

Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val Glu
 465 470 475 480

Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly Glu
 485 490 495

Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr Glu
 500 505 510

Asn Thr His Ile Tyr
 515

<210> 9
 <211> 37
 <212> DNA
 <213> Chlamydia muridium

<400> 9
 ataagaatgc ggccgcatgc gaataggaga tcctatg

37

<210> 10
 <211> 37
 <212> DNA
 <213> Chlamydia muridium

<400> 10
cgaccaagc ttcataagata tgtgtattct ccgtatc 37

<210> 11
<211> 40
<212> DNA
<213> Chlamydia muridum

<400> 11
ataagaatgc ggccgcatgg agtctctctc taccaacgtt 40

<210> 12
<211> 37
<212> DNA
<213> Chlamydia muridum

<400> 12
cgaccaagc ttcataagata tgtgtattct ccgtatc 37

<210> 13
<211> 31
<212> DNA
<213> Chlamydia muridum

<400> 13
gaattcggat ccgatgaaca aactcatcag a 31

<210> 14
<211> 36
<212> DNA
<213> Chlamydia muridum

<400> 14
attaagaatg cggccgcttc attaatagat atgtgt 36